```
  GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCC
1 ---------+---------+---------+---------+---------+---------+ 60

   ATCCGAAAGAGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
61 ---------+---------+---------+---------+---------+---------+ 120

    AGTCAGAGACCCTCCTGAAAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGG
121 ---------+---------+---------+---------+---------+---------+ 180

    CTGCGGCCCCTCCGTTCTTTCCCCCTCCCCGAGAGACACTCTTCCTTTCCCCCCACGAAG
181 ---------+---------+---------+---------+---------+---------+ 240

    ACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCCATGGGAGGCCGCTTCCTGCTGACG
241 ---------+---------+---------+---------+---------+---------+ 300
```

FIG. 1A

```
    CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGGTGTTCGAG
301 ---------+---------+---------+---------+---------+---------+ 360

    CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG
361 ---------+---------+---------+---------+---------+---------+ 420

    GGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC
421 ---------+---------+---------+---------+---------+---------+ 480

    TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
481 ---------+---------+---------+---------+---------+---------+ 540

    ATCACCCCCGTCCTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGAC
541 ---------+---------+---------+---------+---------+---------+ 600

    CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG
601 ---------+---------+---------+---------+---------+---------+ 660

    CTCATCATCGAGGCTCTGCACACCGACTCCCCCGACGACCTCACCACAGAAAACCCCGAG
661 ---------+---------+---------+---------+---------+---------+ 720
```

FIG. 1A (cont'd)

721 CGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG 780

781 GACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTTGTGTGTGATGAG 840

841 CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC 900

901 TTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGC 960

961 ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGG 1020

1021 GAATGCAAGTGCAGAGTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA 1080

1081 GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGC 1140

FIG. 1A (cont'd)

```
     GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200

1201 ---------+---------+---------+---------+---------+---------+ 1260
     CGGTGTACGTGGTTGTGGCCAGTCCCCTCCATGTGAACAAGAACGGCTGGACCCATGTGT

     GGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA
1261 ---------+---------+---------+---------+---------+---------+ 1320

     AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380

     AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC
1381 ---------+---------+---------+---------+---------+---------+ 1440

     ACTGACAACCCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500

     TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT
1501 ---------+---------+---------+---------+---------+---------+ 1560
```

FIG. 1A (cont'd)

```
     GACCTGGGGAACTCCTACATATGCCAGTGCCAGGCTGGCTTCACTGGCAGGCACTGTGAC
1561 ---------+---------+---------+---------+---------+---------+ 1620

     GACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTCAATGGAGGGACCTGTCAGGATGGG
1621 ---------+---------+---------+---------+---------+---------+ 1680

     GTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681 ---------+---------+---------+---------+---------+---------+ 1740

     GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741 ---------+---------+---------+---------+---------+---------+ 1800

     CGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801 ---------+---------+---------+---------+---------+---------+ 1860

     GAGCCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861 ---------+---------+---------+---------+---------+---------+ 1920

     AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTG
1921 ---------+---------+---------+---------+---------+---------+ 1980
```

FIG. 1A (cont'd)

```
                TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401 ----------+----------+----------+----------+----------+----------+ 2460

                TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461 ----------+----------+----------+----------+----------+---------- 2508
```

FIG. 1A (cont'd)

1 GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCCATCCGAAAG 69

70 AGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAACAGTCAGAGACCCTCCTGA 138

139 AAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGGCTGCGGCCCCTCCGTTCTTTCCCCCTC 207

208 CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCC 276

277 ATGGGAGGCCGCTTCCTGCTGACGCTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGC 345

346 TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGC 414

415 TGCCGGGGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTCTGC 483

FIG. 1B

484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCA

553 CTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGACCCCGCCTTCA

622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGC

691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGA

760 GTGGGCGAGGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCGACCTCAAGTAC

FIG. 1B (cont'd)

GTGTGATGAGCACTACTACGGCGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGT 897

898(CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG 966

967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035

1036 GTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCAGGCTGCCTGCACGGTACCTGTCAG 1104

1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173

1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGAGCTACACTTGTTCT 1242

1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAG 1311

FIG. 1B (cont'd)

1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA 1380

1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449

1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518

1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587

1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTC 1656

1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725

FIG. 1B (cont'd)

1726 AACTGCAGCACGCCGGTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794

1795 AGCAACCGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCCGAG 1863

1864 CCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932

1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001

2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCACCATCAGCCGGAGTCCTGCAGGAGTGAAACGGAGACCATG 2070

2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139

2140 AACACAAATAAGAAAGTAGACTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208

FIG. 1B (cont'd)

2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277

2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCGCAGTACAGCTAAAAAGTAGTGAC 2346

2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415

2416 GTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTTAGTATCCCACCTGGCAGTCGGACA 2484

2485 AGTCTTGGTGTGTGATTCCCATCCAGCGCAGGTCAGGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553

2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622

FIG. 1B (cont'd)

2623 ATTAACATAAGCTCCAGTGGGGGTTACAGGGACAGCAATTTTTGCAGGCAAGGGTATAACTGTAGTGCA 2691

2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760

2761 TTGAGGTGAAGTCCTGACCCTCTGCATCCTCATAGTCCTCTGCTTTCTTTTTATTAACCTCTTCTGGTC 2829

2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAACAGACGTGACGTGCCAAAGCTT 2883

FIG. 1B (cont'd)

```
  1 MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
 61 DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRTDLKY
181 SYRFVCDEHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCKNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQCQA GFTGRHCDDN VDDCASFPCV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPSVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAEE KSAVQLKSSD TSERKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV
```

FIG. 2

```
C-Delta-1    1  MGGRFLLTLA-LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC   60
X-Delta-1    1  MGQQRMLTLL-VLSAVL--CQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSL--ASLQRC   56
Delta        1  --MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG   59

C-Delta-1   61  DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPPFGP  121
X-Delta-1   57  ECKTFFRICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPES-SNADPTFSNPIRFPPFGP  116
Delta       60  SCKTRFRLCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPPFSF  120

C-Delta-1  122  TWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY  182
X-Delta-1  117  TWPGTFSLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSY  177
Delta      121  SWPGTFSLIVEAWH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF  180

C-Delta-1  183  RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGF  243
X-Delta-1  178  RFVCDEYYYGEGCSDYCRPRDDAFGHFSCGERGEKLCNPGWKGLYCTEPICLPGCDEHHGY  238
Delta      181  RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGH  239
                   <------------------------ DSL ------------------><-----------

C-Delta-1  244  CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP  304
X-Delta-1  239  CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP  299
Delta      240  CDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP  300
                EGF1 ---------------><----------- EGF2 ------------------><------

C-Delta-1  305  CKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDA--NPCKNGGSCTD---LENSYSCT  360
X-Delta-1  300  CENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDA--NPCKNGGSCSD---LENSYTCS  355
Delta      301  CKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCH  361
                ---- EGF3 -------------------><---------------- EGF4 ----------

C-Delta-1  361  CPPGFYGKNCELSAMTCADGPCFNG-----GRCTDNPDGGYSCRCPLGYSGFNCEKKIDYC  416
X-Delta-1  356  CPPGFYGKNCELSAMTCADGPCFNG-----GRCADNPDGGYICFCPGVYSGFNCEKKIDYC  411
Delta      362  CRNGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNC  422
                -------><-------------------- EGF5 -------------------><------

C-Delta-1  417  SSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCP  477
X-Delta-1  412  SSNPCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCP  472
Delta      423  SPNPCINGGSCQPSGK---CICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV  480
                ------ EGF6 -------------------><--------------- EGF7 ----------

C-Delta-1  478  PGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP----  534
X-Delta-1  473  PGYIGKNCSMPITKCEHNPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPE---------  524
Delta      481  PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHNG  541
                -------><------------ EGF8 ------------------------------------

C-Delta-1  535  ---------------------------VIVDFTE--KYTEGQNSQFPW--IAVCAGIILVL  564
X-Delta-1  525  ------------------------EKPVVVDLTE--KYTEGQSGQFPW--IAVCAGIVLVL  557
Delta      542  GTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQVVLIAVFS  602
                --- EGF9 --------------->                             ----------

C-Delta-1  565  MLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKD--ISISVIGATQIKNT  623
X-Delta-1  558  MLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMNNLANCQREKD--ISVSFIGTTQIKNT  616
Delta      603  VAMPLVAVIAACVVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHHNGSAVGVALASASMG  663
                -- TM -----------

C-Delta-1  624  NKKVDFHSD-NSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAKCETYDSEAEEKSA  683
X-Delta-1  617  NKKIDFLSESNNEKNGYKPRYPSVDYNLVHELKNEDSPKEERSKCEAKCSSNDSDSEDVNS  677
Delta      664  GKTGSNSGLTFDGGNPNIIKNTWDKSVN-NICASAAAAAAAAAAAADECLMYGGYVASVADN  723

C-Delta-1  684  -----VQLKSSDTSERK--------RPDSVYSTSKDTKYQSVYYVISEEKDECIIATEV    728
X-Delta-1  678  -----VHSK-RDSSERR--------RPDSAYSTSKDTKYQSVYYVISDEKDECIIATEV    721
Delta      724  NNANSDFCVAPLQRAKSQKQLNTDPTLMHRGSPAGTSAKGASGGGPGAAEGKRISVLGEGS  784

Delta      785  YCSQRWPSLAAAGVAGACSSQLMAAASAAGTDGTAQQQRSVVCGTPHM               832
```

FIG. 3

```
C-Delta-1     184  V-CDEHYYGE G-CSVFCRPR DDRFGHFTCG ERGEKVCNPG WKGQYC  228
Delta         182  VTCDLNYYGS G-CAKFCRPR DDSFGHSTCS ETGEIICLTG WQGDYC  226
Serrate       235  VQCAVTYYNT TFCTTFCRPR DDQFGHYACG SEGQKLCLNG WQGVNC  279
C-Serrate-1        VTCAEHYYGF G-CNKFCRPR DDFFTHHTCD QNGNKTCLEG WTGPEC

apx-1         130  NLCSSNYHGK R-CNRYCIAN -AKLHWE-CS THGVRRCSAG WSGEDC  172
lag-2         120  VTCARNYFGN R-CENFCDAH LAKAARKRCD AMGRLRCDIG WMGPHC  166
```

FIG. 4

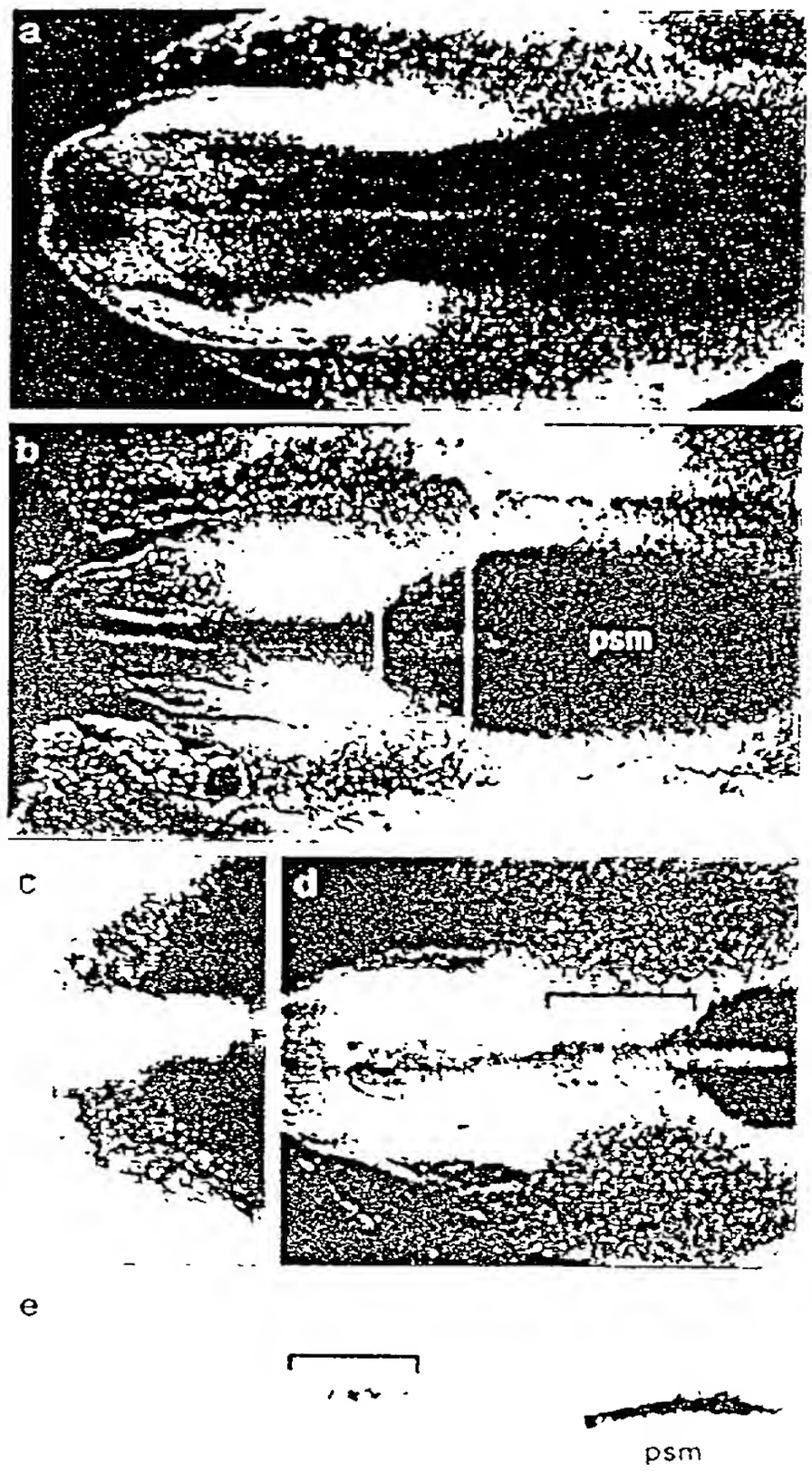

FIG. 5

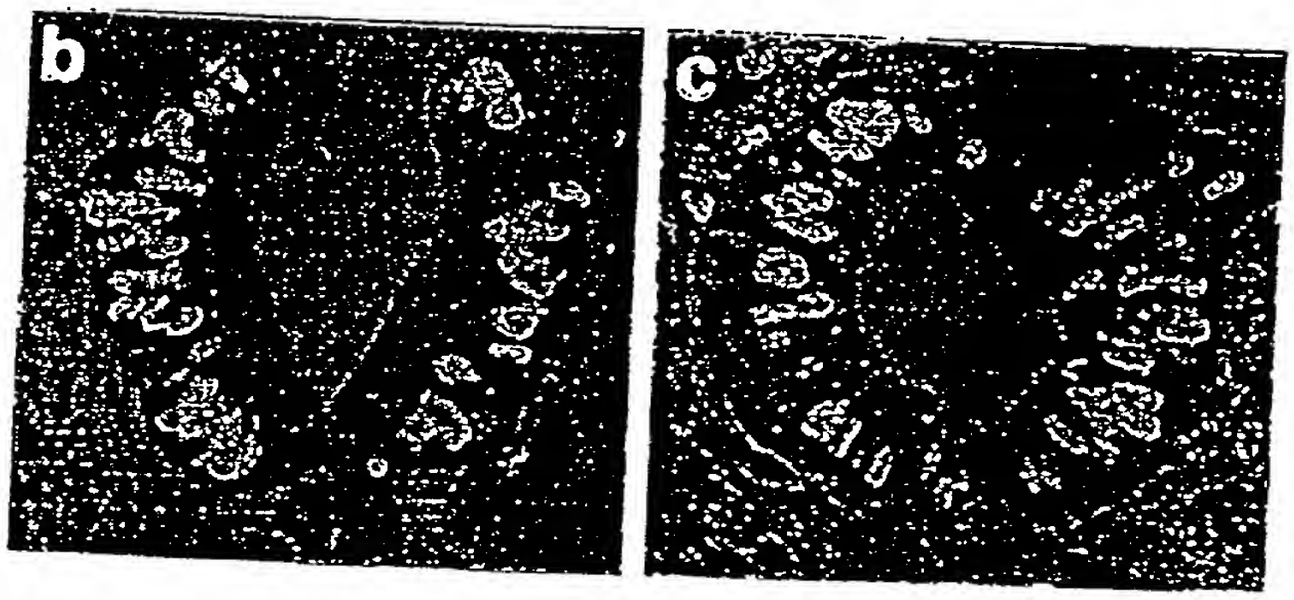

FIG. 6B FIG. 6C

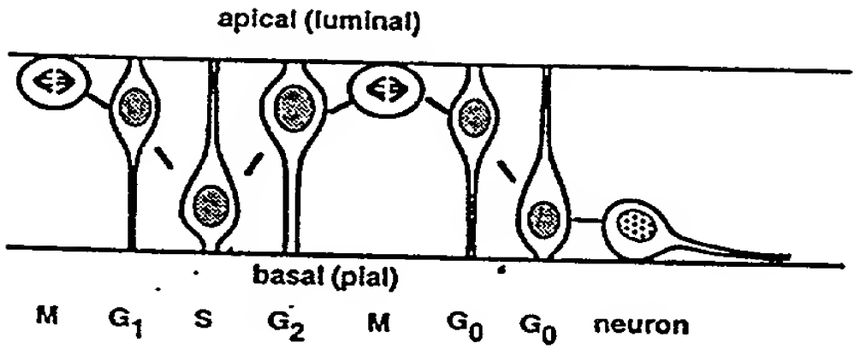

FIG. 6A

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT      60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG     120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT     180
GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC TCAAGCACTA CCAGGCCAGC     240
GTGTCACCGG AGCCACCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTCGAC     300
TCCTTCAGCC TGCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC     360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC     420
TCTCCCGATG ACCTCGCAAC AGAAAACCCA GAAAGACTCA TCAGCCGCCT GACCACACAG     480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC     540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG     600
TTCTGCCGAC CTCGGGATGA CGCCTTTGGC CACTTCACCT GCGGGGACAG AGGGGAGAAG     660
ATGTGCGACC CTGGCTGGAA AGGCCAGTAC TGCACTGACC CAATCTGTCT GCCAGGGTGT     720
GATGACCAAC ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAGAGT TGGCTGGCAG     780
GGCCGCTACT GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA     840
CCCTGGCAGT GTAACTGCCA GGAAGGCTGG GGGGGCCTTT TCTGCAACCA AGACCTGAAC     900
TACTGTACTC ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCCAGGGG     960
AGCTACACAT GTTCCTGCCG ACCTGGGTAT ACAGGTGCCA ACTGTGAGCT GGAAGTAGAT    1020
GAGTGTGCTC CTAGCCCCTG CAAGAACGGA GCGAGCTGCA CGGACCTTGA GGACAGCTTC    1080
TCTTGCACCT GCCCTCCCGG CTTCTATGGC AAGGTCTGTG AGCTGAGCGC CATGACCTGT    1140
GCAGATGGCC CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC    1200
TGCCATTGCC CCTTGGGCTT CTCTGGCTTC AACTGTGAGA AGAAGATGGA TCTCTGCGGC    1260
TCTTCCCCTT GTTCTAACGG TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG    1320
TGCCAGGCTG GCTTCTCCGG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC    1380
CCGTGTGCAA ATGGGGGCAC CTGCCGGGAC AGTGTGAACG ACTTCTCCTG TACCTGCCCA    1440
CCTGGCTACA CGGGCAAGAA CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC    1500
CATAATGGGG CCACCTGCCA CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC    1560
TATGGCGGCC CCAACTGCCA GTTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG    1620
GACCTCAGTG AGAGGCATAT GGAGAGCCAG GGCGGGCCCT TCCCCTGGGT GGCCGTGTGT    1680
GCCGGGGTGG TGCTTGTCCT CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC    1740
CGGCTGAAGC TACAGAAACA CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC    1800
ATGAACAACC TAGCCAATTG CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT    1860
ACCCAGATCA AGAACACCAA CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCGAGAAG    1920
AGCAGCTTTA AGGTCCGATA CCCCACTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA    1980
GATGAAGCCA CGGTCAGGGA TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC    2040
TCTGCAGGAG AAGAGAAGAT CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA    2100
AGGCCAGAGT CTGTCTACTC TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG    2160
TCTGCAGAAA AGGATGAGTG TGTTATAGCG ACTGAGGTGT AAGATGGAAG CGATGTGGCA    2220
AAATTCCCAT TTCTCTTAAA TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA    2280
GAGGAAGGGA GAGGAAACCC AGGGACTGCT GCTGAGAACC AGGTTCAGGC GAACGTGGTT    2340
CTCTCAGAGT TAGCAGAGGC GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT    2400
GCCTGCTGGT TGTTCCCATT GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG    2460
GACGAGTGAC TTGATTCATA TAGGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT    2520
ATGAGCCAGT CTTTCCTTGA ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG    2580
AGATGTGTTT TTTTTTTTTC CTAGACGGGA AAAAGAAAAC GTGTGTTATT TTTTTTGGGA    2640
TTTGTAAAAA TATTTTTCAT GATTATGGGA GAGCTCCCAA CGCGTTGGAG GT            2692
```

FIG. 7

MGRRSALALA	VVSALLCQVW	SSGVFELKLQ	EFVNKKGLLG	NRNCCRGGSG	50
PPCACRTFFR	VCLKHYQASV	SPEPPCTYGS	AVTPVLGVDS	FSLPDGAGID	100
PAFSNPIRFP	FGFTWPGTFS	LIIEALHTDS	PDDLATENPE	RLISRLTTQR	150
HLTVGEEWSQ	DLHSSGRTDL	RYSYRFVCDE	HYYGEGCSVF	CRPRDDAFGH	200
FTCGDRGEKM	CDPGWKGQYC	TDPICLPGCD	DQHGYCDKPG	ECKCRVGWQG	250
RYCDECIRYP	GCLHGTCQQP	WQCNCQEGWG	GLFCNQDLNY	CTHHKPCRNG	300
ATCTNTGQGS	YTCSCRPGYT	GANCELEVDE	CAPSPCKNGA	SCTDLEDSFS	350
CTCPPGFYGK	VCELSAMTCA	DGPCFNGGRC	SDNPDGGYTC	HCPLGFSGFN	400
CEKKMDLCGS	SPCSNGAKCV	DLGNSYLCRC	QAGFSGRYCE	DNVDDCASSP	450
CANGGTCRDS	VNDFSCTCPP	GYTGKNCSAP	VSRCEHAPCH	NGATCHQRGQ	500
RYMCECAQGY	GGPNCQFLLP	EPPPGPMVVD	LSERHMESQG	GPFPWVAVCA	550
GVVLVLLLLL	GCAAVVVCVR	LKLQKHQPPP	EPCGGETETM	NNLANCQREK	600
DVSVSIIGAT	QIKNTNKKAD	FHGDHGAEKS	SFKVRYPTVD	YNLVRDLKGD	650
EATVRDTHSK	RDTKCQSQSS	AGEEKIAPTL	RGGEIPDRKR	PESVYSTSKD	700
TKYQSVYVLS	AEKDECVIAT	EV			722

FIG. 8

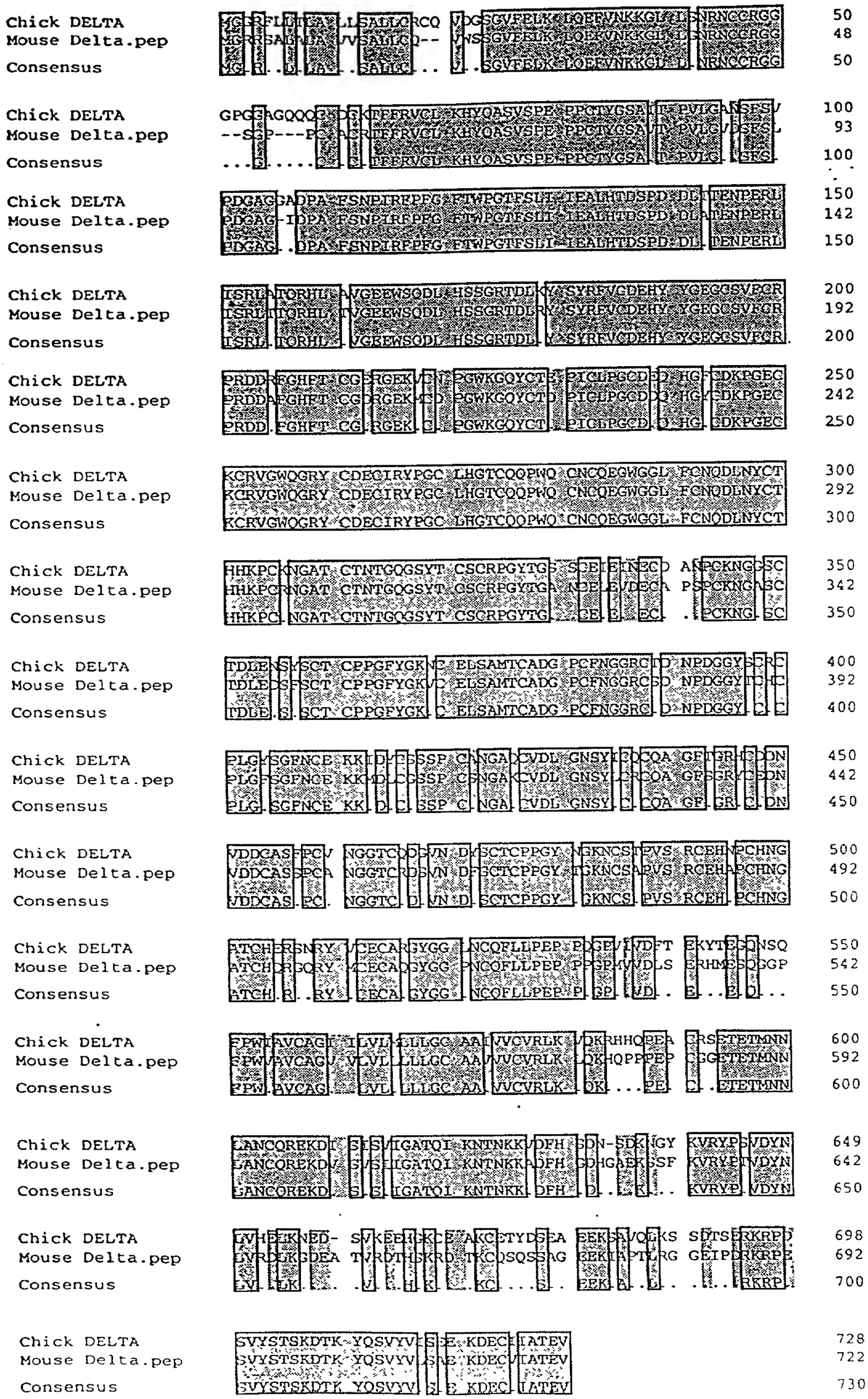
Chick DELTA
Mouse Delta.pep
Consensus
50
48
50
100
93
100
150
142
150
200
192
200
250
242
250
300
292
300
350
342
350
400
392
400
450
442
450
500
492
500
550
542
550
600
592
600
649
642
650
698
692
700
728
722
730

FIG. 9

```
        10          20          30          40          50          60
                    *           *                       *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TGAGAAGGAC ATCTCAGTCA GCATCATCGG
 Y  D  E   X  P  G  E   L  P  A   *  E  G   H  L  S  Q   H  H  R>
  T  M  N   N  L  A   N  C  Q  R   E  K  D   I  S  V   S  I  I  G>
   R  *  X   T  W  R   T  A  S   V  R  R  T   S  Q  S   A  S  S>

        70          80          90          100         110         120
                    *           *                       *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG
 G  X  V   R  S  X  T   P  T  R   R  R  T   X  X  R  G   T  X  A>
  A  T  S   D  Q  E   H  Q  Q  E   G  G  L   X  X  G  G   P  X  R>
G  X  R  Q   I  X  N   T  N  K   K  A  D  F   X  X  G   D  X  S>

        130         140         150         160         170         180
                    *           *                       *
TCCGACAAGA ATGGMTTTCA AGGCCCGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC
 S  D  K   N  G  F  Q   G  P  L   P  Q  R   G  L  *  L   V  Q  D>
  P  T  R   M  X  F   K  A  R  Y   P  S  V   D  Y  N   S  C  R  T>
V  R  Q  E   W  X  S   R  P  A   T  P  A  W   T  I  T   R  A  G>

        190         200         210         220         230         240
                    *           *                       *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG
 L  K  G   D  D  T  A   V  R  T   S  H  S   K  R  D  T   K  C  Q>
  S  R  V   T  T  P   P  S  G  R   R  T  A   S  V  T   P  S  A  S>
P  Q  G  *   R  H  R   R  Q  D   V  A  Q  Q   A  *  H   Q  V  P>

        250         260         270         280         290         300
                    *           *                       *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCGACCAC ACTCAGGGGK TGCGTGCTGC
 S  P  G   S  S  G  R   R  R  G   P  R  P   H  S  G  X   A  C  C>
  P  Q  A   P  Q  G   G  E  G  D   P  D  H   T  Q  G   X  R  A  A>
V  P  R  L   L  R  E   E  K  G   T  P  T  T   L  R  G   C  V  L>

        310         320         330         340         350         360
                    *           *                       *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG 'GTGTCTTCCT GGAACCACTG CTCCGTTTCT
 G  P  G   S  G  G  G   T  W  G   V  S  S   W  N  H  C   S  V  S>
  G  R  A   Q  E  G   V  P  G  G . C  L  P   G  T  T  A   P  F  L>
R  A  G  L   R  R  G   Y  L  G   G  V  F  L   E  P  L  L   R  F>
```

FIG. 10

```
          370         380         390         400         410         420
                      *           *                       *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA
 L  P  K    C  S  H  A    F  I  V    D  F  L    Y  F  P  F    S  G  E>
   F  P  N    V  L  M    H  S  L  W    I  F  S    I  F  L    L  V  E  K>
S  S  Q  M    F  S  C    I  H  C    G  F  S  L    F  S  F    *  W  R>

          430         440         450         460         470         480
                      *           *                       *
GCATCTGAAA GAAAAAGGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG
 A  S  E    R  K  R  P    D  S  G    C  S  T    S  K  D  T    K  Y  Q>
   H  L  K    E  K  G    R  T  R  A    V  Q  L    Q  K  T    P  S  T  S>
S  I  *  K    K  K  A    G  L  G    L  F  N  F    K  R  H    Q  V  P>

          490         500         510         520
                      *           *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA
 S  V  Y    V  I  S  E    E  K  D    E  C  V    I  A>
   R  C  T    S  Y  P    R  R  R  T    S  A  S    S>
V  G  V  R    H  I  R    G  E  G    R  V  R  H    R>
```

FIG. 10 (cont'd)

```
  1 TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY 50
    ||||||||||||||||:|:|||||| |||||.||   ::   |||||: |.||
597 TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDN..SDKNGY.KVRY 643

 51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC 100
    ||||||||::||.:| .|:..|:| :.||:. :|.:  :::
644 PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA......... 683

101 GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG 150
                                |::     |::.||||||||.
684 ............................VQLK....SSDTSERKRPDSV 700

151 CSTSKDTKYQSVYVISEEKDECVIA 175
    :||||||||||||||||||||:||
701 YSTSKDTKYQSVYVISEEKDECIIA 725
```

FIG. 11

```
        10          20          30          40          50          60
    *   *   *   *   *   *   *   *   *   *   *   *
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG

        70          80          90          100         110         120
    *   *   *   *   *   *   *   *   *   *   *   *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA

        130         140         150         160         170         180
    *   *   *   *   *   *   *   *   *   *   *   *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT

        190         200         210         220         230         240
    *   *   *   *   *   *   *   *   *   *   *   *
GACGGTGGGC CAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA

        250         260         270         280         290         300
    *   *   *   *   *   *   *   *   *   *   *   *
CTCCTACCGC TTCGTGTGTC ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG

        310         320         330         340         350         360
    *   *   *   *   *   *   *   *   *   *   *   *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA

        370         380         390         400         410         420
    *   *   *   *   *   *   *   *   *   *   *   *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA

        430         440         450         460         470         480
    *   *   *   *   *   *   *   *   *   *   *   *
GCATGGATTT TGTGACAAAC CAGCGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA

        490         500         510         520         530         540
    *   *   *   *   *   *   *   *   *   *   *   *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA

        550         560         570         580         590         600
    *   *   *   *   *   *   *   *   *   *   *   *
GTGCAACTGC CAGGAAGGNT GGGGGCGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC

        610         620         630         640         650         660
    *   *   *   *   *   *   *   *   *   *   *   *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC

        670         680         690         700         710         720
    *   *   *   *   *   *   *   *   *   *   *   *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA

        730         740         750         760         770         780
    *   *   *   *   *   *   *   *   *   *   *   *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC

        790         800         810         820         830         840
    *   *   *   *   *   *   *   *   *   *   *   *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG

        850         860         870         880         890         900
    *   *   *   *   *   *   *   *   *   *   *   *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
```

FIG. 12A

```
      910         920         930         940         950         960
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC

      970         980         990        1000        1010        1020
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG

     1030        1040        1050        1060        1070        1080
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC

     1090        1100        1110        1120        1130        1140
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC

     1150        1160        1170        1180        1190        1200
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCACGTG CGAGCACGCA

     1210        1220        1230        1240        1250        1260
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC

     1270        1280        1290        1300        1310        1320
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CGAAGCTACG GGGGTCCCAA CTCCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA

     1330        1340        1350        1360        1370        1380
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT

     1390        1400        1410        1420        1430        1440
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTC CTGGGCTGTG CCGCTGTGGT

     1450        1460        1470        1480        1490        1500
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA

     1510        1520        1530        1540        1550        1560
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT

     1570        1580        1590        1600        1610        1620
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG

     1630        1640        1650        1660        1670        1680
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA

     1690        1700        1710        1720        1730        1740
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
CCTCAAGGGT GACGACACCG CCGTCAGCGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA

     1750        1760        1770        1780        1790        1800
    *   *     *   *     *   *     *   *     *   *     *   *     *   *
GCCCCAGGGC TCCTCAGGGG AGGACAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG

     1810        1820        1830        1840        1850        1860
    *   *     *   *     *   *                                 *   *
```

FIG. 12A (cont'd)

```
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA

      1870       1880       1890       1900       1910       1920
   *     *     *     *     *     *     *     *     *     *     *     *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG

      1930       1940       1950       1960       1970       1980
   *     *     *     *     *     *     *     *     *     *     *     *
AGGTNGTAAA NTCGNAGTTG ANNTTGCAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT

T
```

FIG. 12A (cont'd)

```
        10         20         30         40         50         60
        *  *       *  *       *  *       *  *       *  *       *  *   a.a. no.
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
 H  W  V   R  A  P  L   E  V  D   G  I  D   K  L  D  I   E  F  R>  20
  I  G  Y   G  P  P  S   R  S  T   V  S  I   S  L  I  S   N  S [G>] 20
   L  G  T   G  P  P  R   G  R  R   Y  R  *   A  *  Y  R   I  P>  19

        70         80         90        100        110        120
        *  *       *  *       *  *       *  *       *  *       *  *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
 L  H  L   A  G  H  L   L  S  D   Y  *  S   S  P  H  R   F  S  *>  40
[ F  T  W   P  G  T  F   S  L  I   I  E  A   L  H  T  D   S  P  D>] 40
 A  S  P   G  R  A  P   S  L  *   L  L  K   L  S  T  Q   I  L  L>  39

       130        140        150        160        170        180
        *  *       *  *       *  *       *  *       *  *       *  *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
 *  P  R   N  R  K  P   R  K  T   H  Q  P   P  G  H  P   E  A  P>  60
[ D  L  A   T  E  N  P   E  R  L   I  S  R   L  A  T  Q   R  H  L>] 60
 M  T  S   Q  Q  K  T   Q  K  D   S  S  A   A  W  P  P   R  G  T>  59

       190        200        210        220        230        240
        *  *       *  *       *  *       *  *       *  *       *  *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
 D  G  G   R  G  V  V   P  G  P   A  Q  Q   R  P  H  G   P  Q  V>  80
[ T  V  G   E  E  W  S   Q  D  L   H  S  S   G  R  T  D   L  K  Y>] 80
 *  R  W   A  R  S  G   P  R  T   C  T  A   A  A  A  R   T  S  S>  79

       250        260        270        280        290        300
        *  *       *  *       *  *       *  *       *  *       *  *
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
 L  L  P   L  R  V  *   R  T  L   L  R  R   G  L  L  R   F  L  P>  100
[ S  Y  R   F  V  C  D   E  H  Y   Y  G  E   G  C  S  V   F  C  R>] 100
 T  P  T   A  S  C  V   T  N  T   T  T  E   R  A  A  P   F  S  A>  99

       310        320        330        340        350        360
        *  *       *  *       *  *       *  *       *  *       *  *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
 S  P  G   R  C  L  R   P  L  H   L  W  G   A  W  G  E   S  V  Q>  120
[ P  R  D   D  A  F  G   H  F  T   C  G  E   R  G  E  K   V  C  N>] 120
 V  P  G   T  M  P  S   A  T  S   P  V  C   S  V  G  R   K  C  A>  119

       370        380        390        400        410        420
        *  *       *  *       *  *       *  *       *  *       *  *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
 P  W  L   E  R  A  L   L  H  R   A  D  L   P  A  W  M   *  *  A>  140
[ P  G  W   K  G  P  Y   C  T  E   P  I  C   L  P  G  C   D  E  Q>] 140
 T  L  A   G  K  G  P   T  A  Q   S  R  S   A  C  L  D   V  M  S>  139

       430        440        450        460        470        480
        *  *       *  *       *  *       *  *       *  *       *  *
GCATGGATTT TGTGACAAAC CAGCCCAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
 A  W  I   L  *  Q  T   R  G  M   Q  V  Q   S  G  L  A   G  P  V>  160
[ H  G  F   C  D  K  P   G  E  C   K  C  R   V  G  W  Q   G  R  Y>] 160
 S  M  D   F  V  T  N   Q  G  N   A  S  A   E  W  A  G   R  A  G>  159

       490        500        510        520        530        540
        *  *       *  *       *  *       *  *       *  *       *  *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
 L  *  R   V  Y  P  L   S  R  L   S  P  W   H  L  P  A   A  L  A>  180
```

FIG. 12B

```
  C  D  E  C  I  R  Y  P  G  C  L  H  G  T  C  Q  Q  P  W  Q>  180
  T  V  T  S  V  S  A  I  Q  A  V  S  M  A  P  A  S  S  P  G>  179

        550       560       570       580       590       600
     *  *  *  *  *  *  *  *  *  *  *  *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTCTGCAAC CAGGACCTGA ACTACTGCAC
 V  Q  L  P  G  R  X  G  G  P  F  L  Q  P  G  P  E  L  L  H>  200
 C  N  C  Q  E  G  W  G  G  L  F  C  N  Q  D  L  N  Y  C  T>  200
S  A  T  A  R  K  X  G  G  A  F  S  A  T  R  T  *  T  T  A>  199

        610       620       630       640       650       660
     *  *  *  *  *  *  *  *  *  *  *  *
ACACCATAAG CCCTGCAAGA ATCCAGCCAC CTGCAACAAA CACGGCCCAG GGGGAGCTAC
 T  P  *  A  L  Q  E  W  S  H  L  Q  Q  T  R  A  R  G  S  Y>  220
 H  H  K  P  C  K  N  G  A  T  C  N  K  H  G  P  G  C  A  T>  220
H  T  I  S  P  A  R  M  E  P  P  A  T  N  T  G  Q  G  E  L>  219

        670       680       690       700       710       720
     *  *  *  *  *  *  *  *  *  *  *  *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
 T  W  S  L  A  G  L  G  Y  X  G  C  H  L  R  S  L  G  I  G>  240
 L  G  L  W  P  X  W  G  T  X  G  A  T  C  E  A  W  G  L  D>  240
H  L  V  F  G  R  X  G  V  X  R  V  P  P  A  K  L  G  D  W>  239

        730       740       750       760       770       780
     *  *  *  *  *  *  *  *  *  *  *  *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
 R  V  V  D  P  S  P  W  *  E  R  R  E  L  D  G  S  S  E  N>  260
 E  L  L  T  P  A  L  G  K  N  G  G  S  L  T  D  L  R  R  T>  260
T  S  C  *  P  Q  P  L  V  R  T  E  Q  A  *  R  I  F  G  E>  259

        790       800       810       820       830       840
     *  *  *  *  *  *  *  *  *  *  *  *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
 S  Y  S  C  T  C  P  P  G  F  Y  G  K  I  C  E  L  S  A  M>  280
 A  T  P  V  P  A  H  P  A  S  T  A  K  S  V  N  *  V  P  *>  280
Q  L  L  L  Y  L  P  T  R  L  L  R  Q  N  L  *  I  E  C  H>  279

        850       860       870       880       890       900
     *  *  *  *  *  *  *  *  *  *  *  *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CACACAGCCC CGATGGAGGG
 T  C  A  D  G  P  C  F  N  G  G  R  C  S  D  S  P  D  G  G>  300
 P  V  R  T  A  L  A  L  T  G  V  G  A  Q  T  A  P  M  E  G>  300
D  L  C  G  R  P  L  L  *  R  G  S  V  L  R  Q  P  R  W  R>  299

        910       920       930       940       950       960
     *  *  *  *  *  *  *  *  *  *  *  *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GCCTTCAACT GTGAGAAGAA AATTGACTAC
 Y  S  C  R  C  P  V  G  Y  S  G  F  N  C  E  K  K  I  D  Y>  320
 T  A  A  A  A  P  W  A  T  P  A  S  T  V  R  R  K  L  T  T>  320
V  Q  L  P  L  P  R  G  L  L  R  L  Q  L  *  E  E  N  *  L>  319

        970       980       990       1000      1010      1020
     *  *  *  *  *  *  *  *  *  *  *  *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTCTGTGG ACCTCGGTGA TGCCTACCTG
 C  S  S  S  P  C  S  N  G  A  K  C  V  D  L  G  D  A  Y  L>  340
 A  A  L  H  P  V  L  M  V  P  S  V  W  T  S  V  M  P  T  C>  340
L  Q  L  F  T  L  F  *  W  C  Q  V  C  G  P  R  *  C  L  P>  339

        1030      1040      1050      1060      1070      1080
     *  *  *  *  *  *  *  *  *  *  *  *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
```

FIG. 12B (cont'd)

```
C R C Q A G F S G R H C D D N V D D C A>  360
  A A A R P A S R G G T V T T T W T T A P>  360
V P L P G R L L C E A L * R Q R G R L R>  359

      1090      1100      1110      1120      1130      1140
    *   *   *   *   *   *   *   *   *   *   *   *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC
S S P C A N G G T C R D G V N D F - S C T>  380
  P P R A P T G A P A G M A * T T S P A P>  380
L L P V R Q R G H L P G W R E R L L L H>  379

      1150      1160      1170      1180      1190      1200
    *   *   *   *   *   *   *   *   *   *   *   *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA
C P P G Y T G R N C S A P A S R C E H A>  400
  A R L A T R A G T A V P P P A G A S T H>  400
L P A W L H G Q E L Q C P R Q Q V R A R>  399

      1210      1220      1230      1240      1250      1260
    *   *   *   *   *   *   *   *   *   *   *   *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC
P C H N G A T C H E R G H R Y X C E C A>  420
  P A T M G P P A T R G A T A I C A S V P>  420
T L P Q W G H L P R E G P P L F V R V C>  419

      1270      1280      1290      1300      1310      1320
    *   *   *   *   *   *   *   *   *   *   *   *
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA
R S Y G G P N C X F L L P E T A P P A P>  440
  E A T G V P T A X S C S P K L P P R P H>  440
P K L R G S Q L P X P A P R N C P P G P>  439

      1330      1340      1350      1360      1370      1380
    *   *   *   *   *   *   *   *   *   *   *   *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
R W W K L P *  K N L K G P G G A H P L G>  460
  G G G N S P K K T * K G R G G P I P L V>  460
T V V E T P L K K P K R A G G P S P W>  459

      1390      1400      1410      1420      1430      1440
    *   *   *   *   *   *   *   *   *   *   *   *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTC CCGCTGTGGT
G R V R R G H P C P H A A A G L C R C G>  480
- D V C A G V I L V L M L L L G C A A V V>  480
W T C A P G S S L S S C C C W A V P L W>  479

      1450      1460      1470      1480      1490      1500
    *   *   *   *   *   *   *   *   *   *   *   *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
G L R P A E A A E A P A P S R P L X G G>  500
V C V R L R L Q K H R P P A D P X R G E>  500
W S A S G * G C R S T G P Q P T P X G G>  499

      1510      1520      1530      1540      1550      1560
    *   *   *   *   *   *   *   *   *   *   *   *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
D G D H E Q P G Q L P A * E G H L S Q H>  520
T E T M N N L X N C Q R E K D I S V S I>  520
R R R P * T T W X T A S V R R T S Q S A>  519

      1570      1580      1590      1600      1610      1620
    *   *   *   *   *   *   *   *   *   *   *   *
```

FIG. 12B (cont'd)

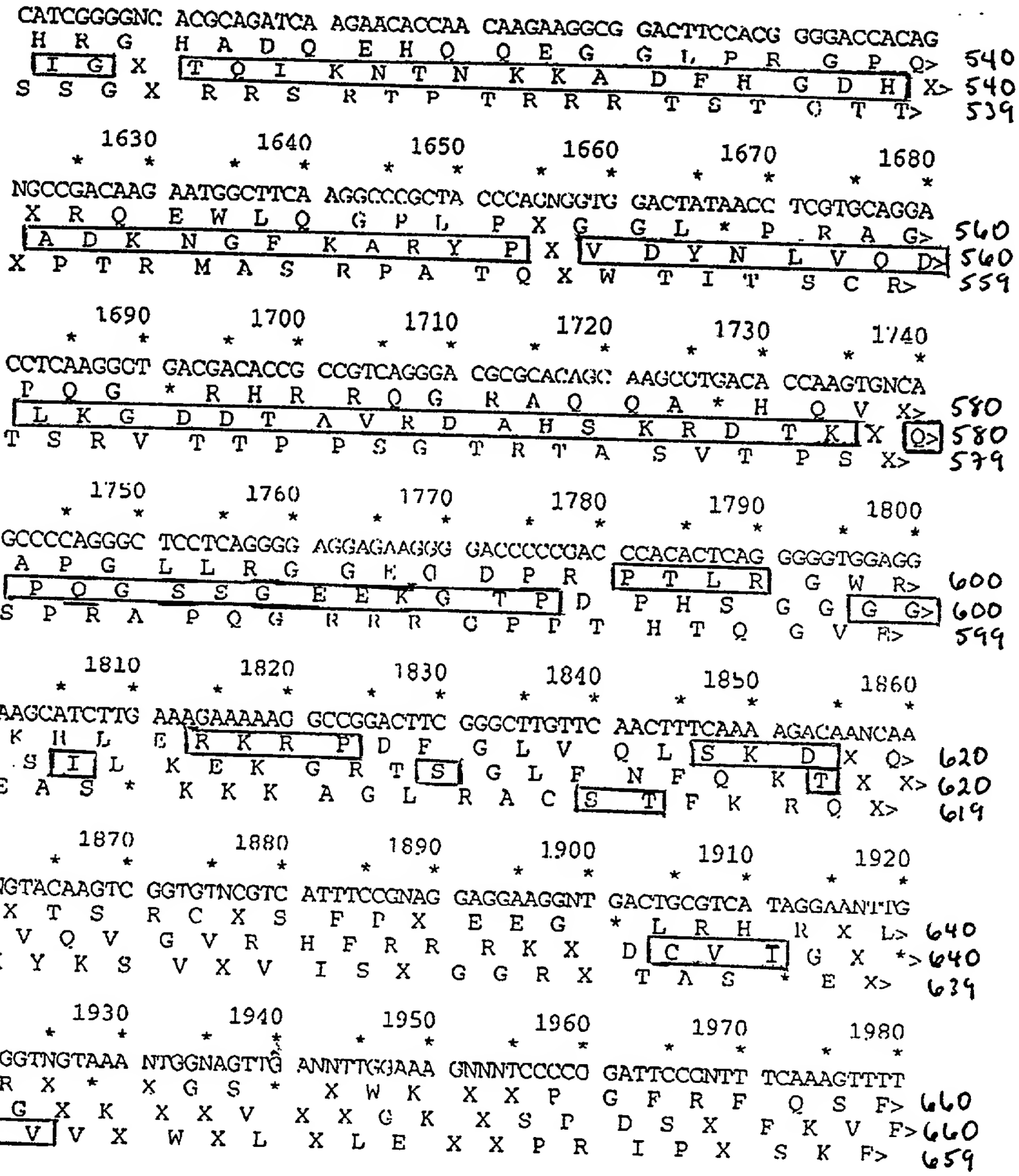

FIG. 12B (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA  GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        GTCCAGCCGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT CCCGTGGTCT   50

Mouse Delta DNA  CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100

Mouse Delta DNA  CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150

Mouse Delta DNA  CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200

Mouse Delta DNA  TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250
Human Delta      ---------- ---------- ---------- ---------- ----------
Consensus        TCAAGCACTA CCAGGCCACC GTGTCACCGG AGCCACCCTG CACCTACGGC  250

Mouse Delta DNA  AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTGATGG  300
Human Delta      ---------- ---------- ---------- ---------- -----CATGG    5
Consensus        AGTGCTGTCA CGCCAGTGCT CCGTGTCGAC TCCTTCAGCC TGCCTSATGG  300

Mouse Delta DNA  CGCAGGCATC GACCGC-- -G CCTTCAGCAA CCCCA--TCC GATGTC-CCC  343
Human Delta      GGTAGGGGCC CGCCTCGAGG TCGACGGTAT CGATAAGCTT GATGTCGAAT   55
Consensus        SGMAGGSRYC SMCCKCGAGG MCKWCRGMAW CSMYAAGYYY GATGTCGMMY  350

Mouse Delta DNA  TCCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATGATTG AAGCCTCCCA  393
Human Delta      TCCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATGATTG AAGCCTCTCA  105
Consensus        TCCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATGATTG AAGCCTCTCA  400

Mouse Delta DNA  TACAGACTCT CCCGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  443
Human Delta      CACAGATTCT CCTGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  155
Consensus        YACAGATCT CCYGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  450

Mouse Delta DNA  GCCGCCTGAC CACACAGAGG CACCTCACTG TGGGCGAAGA CTGGTCTCAG  493
Human Delta      GCCGCCTGCC CACCCAGAGG CACCTGACCG TGGGCGACGA CTGGTCCCAG  205
Consensus        GCCGCCTGRC CACMCAGAGG CACCTSACKG TGGGCGAMGA CTGGTCYCAG  500

Mouse Delta DNA  GACCTTCACA GTAGCGGCCG CACAGACCTC CGGTACTCTT ACCGCTTTGT  543
Human Delta      GACCTGCACA GCAGCGGCCG CACGGACCTC AAGTACTCCT ACCGCTTCGT  255
Consensus        GACCTKCACA GYAGCGGCCG CACRGACCTC MRGTACTCYT ACCGCTTYGT  550

Mouse Delta DNA  GTGTGACGAG CACTACTACG GAGAAGGCTG CTCTGTCTTC TGCCCGACCT C  593
Human Delta      GTGTGACGAA CACTACTACG GAGAGGGCTG CTCCGTCTTC TGCCCGCCCC  305
Consensus        GTGTGACGAR CACTACTACG GAGARGGCTG CTCYGTCTTC TGCCCGACCY C  600

Mouse Delta DNA  GGGATGAGGC CTTTGGCCAC TTCACCTGCG GGGACAGAGG GGAGAAGATG  643
Human Delta      GGGACGATGC CTTCGGCCAC TTCACCTGCG GCGAGCGCGG GGAGAAAGTG  355
Consensus        GGGAMGAMGC CTTYGGCCAC TTCACCTGCG GSGASMGAGG GGAGAARRTG  650
```

FIG. 13

Mouse Delta vs Partial Human Delta

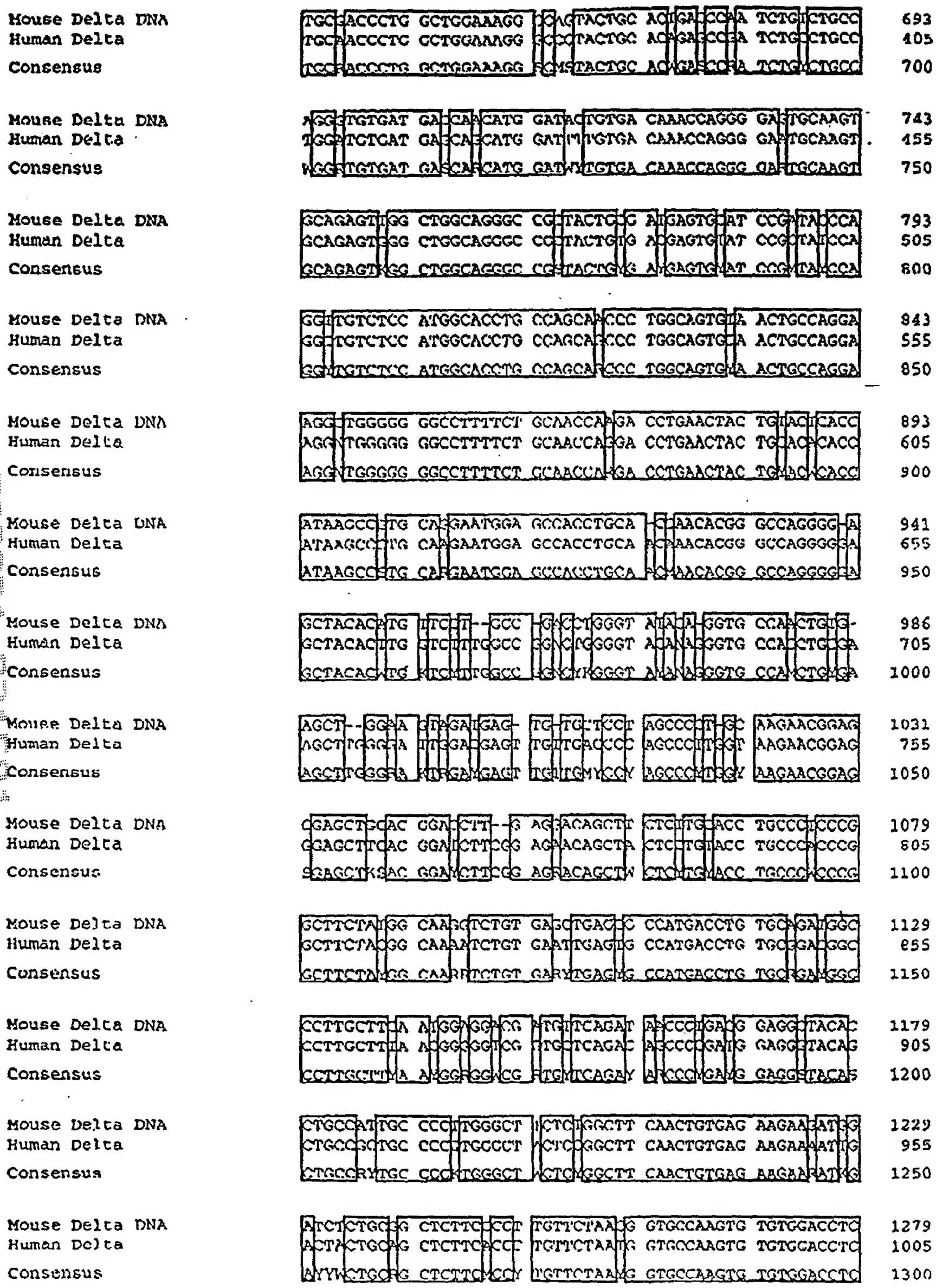

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

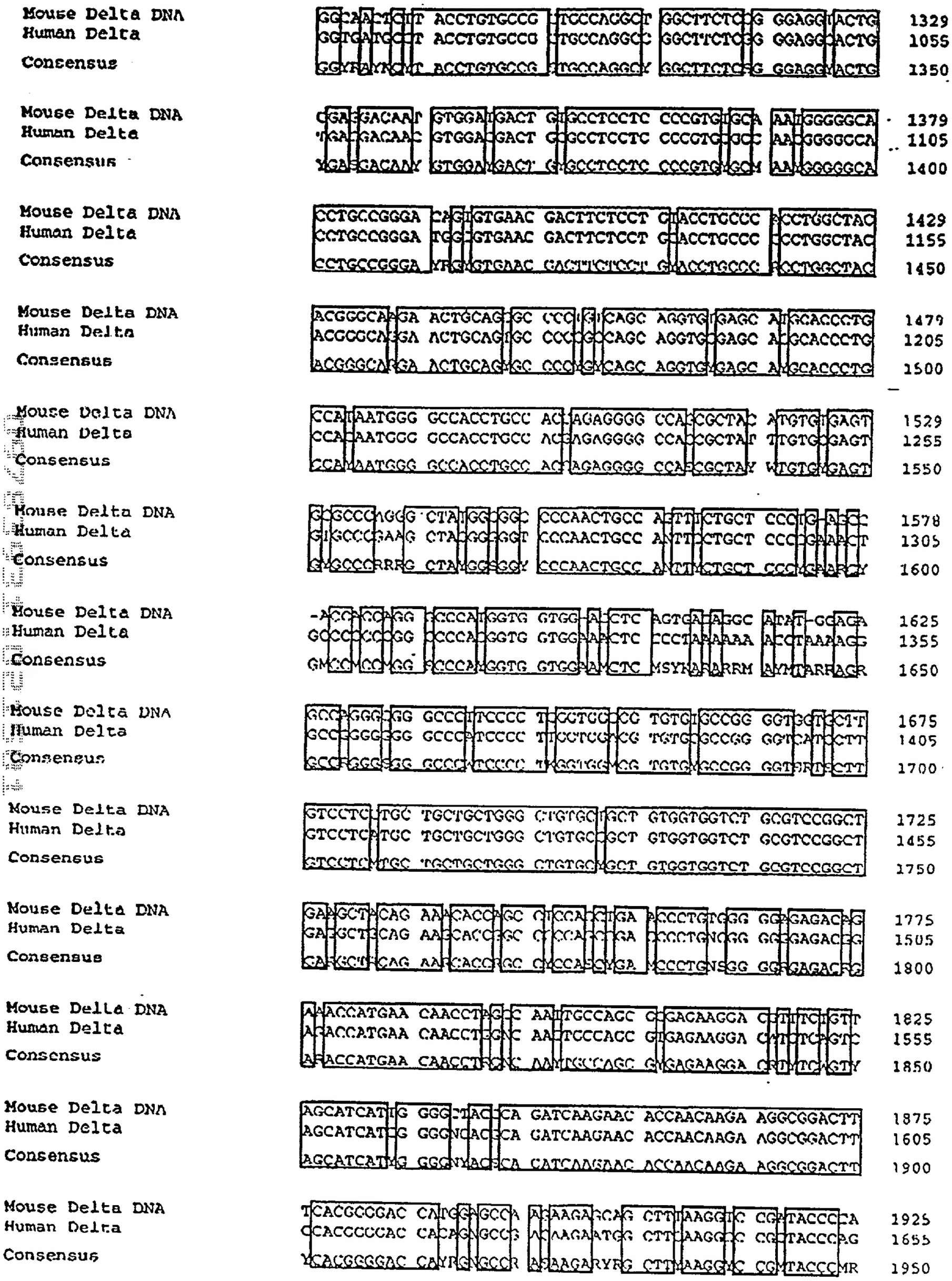

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA   CTGTGGACTA TAACCTCGTT CGAGACCTCA AGGGAGATGA AGCCACGGTC   1975
Human Delta       NGGTGGACTA TAACCTCGTG CAGGACCTCA AGGGTGACGA CACCGCCGTC   1705
Consensus         NKGTGGACTA TAACCTCGTK CRRGACCTCA AGGGAGAMGA MRCCRCSGTC   2000

Mouse Delta DNA   AGGGATACAC ACAGCAAACG TGACACCAAG TGACAGTCAC AGAGCTCTGC   2025
Human Delta       AGGGACCCGC ACAGCAAGCG TCACACCAAG TGCCAGCCGC AGCGCTCCTC   1755
Consensus         AGGGAYRCRC ACAGCAARCG TGACACCAAG TGMCAGYCRC AGMGCTCYKC   2050

Mouse Delta DNA   AGGAGAAGAG AA---GATCG CC--CCAACA CTTA-GGGGT GG-GG-AGAT   2067
Human Delta       ACGGGAGGAG AAGGGGACCC CCGACCCACA CTCAGGGGGT GGAGGAAGCA   1805
Consensus         AGGRGARGAG AAGGGGAYCS CCGACCMACA CTMAGGGGGT GGRGGAAGMW   2100

Mouse Delta DNA   TCCTGACAGA AAAAGGCCAG AGTCT--GTC TACTCTACAT TCAAAGGAC-   2113
Human Delta       TCTTGAAAGA AAAAGGCCGG ACTTCGGGCT TGTTCAACTT TCAAAAGACA   1855
Consensus         TCYTGAMAGA AAAAGGCCRG ASTYYGGGYY TRYTCWACWT TCAAARGACA   2150

Mouse Delta DNA   -ACCAAGTAC CAGTCGGTGT ATGTTCTCTC TGCAGAA--A AGGATGAGTG   2160
Human Delta       ANCAANGTAC AAGTCGGTGT NCGTCATTTC CGNAGGAGGA AGGNTGACTG   1905
Consensus         ANCMANGTAC MAGTCGGTGT NYGTYMTYTC YGNAGRAGGA AGGNTGASTG   2200

Mouse Delta DNA   TGTTATA-GC GACTGAGCT- GTAAGATGGA AGCGATGTGG CAAAATTCCC   2208
Human Delta       CGTCATAGGA ANTTGAGGTN GTAAANTGGN AG---T-TG- --ANNTT---   1945
Consensus         YGTYATAGGM RNYTGAGCTN GTAARNTGGN AGCGATGTGG CAANNTTCCC   2250

Mouse Delta DNA   ATTTCTCTCA AATAAAATTC CAAGGATATA GCCCCGATGA ATGCTCCTGA   2258
Human Delta       -- ----GGA AAGNNN-TC CCCGGAT--- --TCCGNT-- ----TTC---   1972
Consensus         ATTTCTCKSA AAKNNNATTC CMMGGATATA GCYCCGNTGA ATGCTKCTGA   2300

Mouse Delta DNA   GAGACGAAGG GAGAGGAAAC CCACGGACTG CTGCTGAGAA CCAGGTTCAG   2308
Human Delta       -- ------- ------AAA- -------- -G TTTTT----- ----------   1981
Consensus         GAGAGGAAGG GAGAGGAAAC CCAGGGACTG MTKYTGAGAA CCAGGTTCAG   2350

Mouse Delta DNA   GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT   2358
Human Delta       -- ---- - -- ---- -- - -------- ---------- ---- -----   1981
Consensus         GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT   2400

Mouse Delta DNA   AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG   2408
Human Delta       -- ---- -- ---------- ----- --- ---- ----- ----------   1981
Consensus         AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG   2450

Mouse Delta DNA   GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA   2458
Human Delta       ---- ---- --------- --------- - --------- ----------   1981
Consensus         GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA   2500

Mouse Delta DNA   TATACGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA   2508
Human Delta       - ------- ---- ---- ---- ---- --- ----- ----------   1981
Consensus         TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA   2550

Mouse Delta DNA   GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC   2558
Human Delta       ----- --- ---- ----- ---- ---- ---------- ----------   1981
Consensus         GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC   2600
```

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA   TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT  2608
Human Delta       ----------  ----------  ----------  ----------  ----------  1981
Consensus         TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT  2650

Mouse Delta DNA   TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT  2658
Human Delta       ----------  ----------  ----------  ----------  ----------  1981
Consensus         TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT  2700

Mouse Delta DNA   ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA  2708
Human Delta       ----------  ----------  ----------  ----------  ----------  1981
Consensus         ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA  2750

Mouse Delta DNA   AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT  2758
Human Delta       ----------  ----------  ----------  ----------  ----------  1981
Consensus         AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT  2800

Mouse Delta DNA   ATGCAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA  2808
Human Delta       ----------  ----------  ----------  ----------  ----------  1981
Consensus         ATGGAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA  2850

Mouse Delta DNA   AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA   2857
Human Delta       ----------  ----------  ----------  ----------  ---------  1981
Consensus         AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA   2899
```

FIG. 13 (cont'd)

```
G F T W P G T F S L I I E A L H T D S P D> 21
D L A T E N P E R L I S R L A T Q R H L> 41
T V G E E W S Q D L H S S G R T D L K Y> 61
S Y R F V C D E H Y Y G E G C S V F C R> 81
P R D D A F G H F T C G E R G E K V C N> 101
P G W K G P Y C T E P I C L P G C D E Q> 121
H G F C D K P G E C K C R V G W Q G R Y> 141
C D E C I R Y P G C L H G T C Q Q P W Q> 161
C N C Q E G W G G L F C N Q D L N Y C T> 181
H H K P C K N G A T C * T N T G Q G * 198
S Y T * P S P * K N G G S L T D L * 213
E N S Y S C T C P P G F Y G K I C E L S A M> 235
T C A D G P C F N G G R C S D S P D G G> 255
Y S C R C P V G Y S G F N C E K K I D Y> 275
C S S S P C S N G A K C V D L G D A Y L> 295
C R C Q A G F S G R H C D D N V D D C A> 315
S S P C A N G G T C R D G V N D F S C T> 335
C P P G Y T G R N C S A P A S R C E H A> 355
P C H N G A T C H F R G H R Y * C E C A> 374
R S Y G G P N C * F L L P E * P P G P * 391
V V * L L L G C A A V V V C V R L R L Q K H> 412
R P P A D P * R G E T E T M N N L * 428
N C Q R E K D I S V S I I G * T Q I K N T N> 449
K K A D F H G D H * A D K N G F K A R Y P * 469
V D Y N L V Q D L K G D D T A V R D A H S K R D T K * 495
Q P Q G S S G E E K G T P * P T L R * G G * 514
I * R K R P * S * S T * S K D * T * 526
C V I * E V * 531
```

FIG. 14